

## RESULT 1

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 LOCUS Homo sapiens FEZ1 (FEZ1) mRNA, complete cds.  
 DEFINITION AF123659  
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 VERSION human.  
 KEYWORDS  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 5492)  
 AUTHORS Ishii, H., Baffa, R., Numata, S.I., Murakumo, Y., Rattan, S., Inoue, H.,  
 Mori, M., Fidanza, V., Alder, H. and Croce, C.M.  
 TITLE The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,  
 and its expression is altered in multiple human tumors  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)  
 MEDLINE 99199287  
 REFERENCE 2 (bases 1 to 5492)  
 AUTHORS Ishii, H., Baffa, R., Numata, S.I., Murakumo, Y., Rattan, S., Inoue, H.,  
 Mori, M., Fidanza, V., Alder, H. and Croce, C.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer  
 Institute, 233S 10th street, Philadelphia, PA 19107, USA  
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## RESULT 2

AF123653  
 LOCUS Homo sapiens FEZ1 (FEZ1) gene, complete cds. PRI 07-APR-1999  
 DEFINITION AF123653  
 ACCESSION AF123653  
 VERSION AF123653.1 GI:4572463  
 KEYWORDS human.  
 SOURCE ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;  
 Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 9108)  
 AUTHORS Ishii, H., Baffa, R., Numata, S.I., Murakumo, Y., Rattan, S., Inoue, H.,  
 Mori, M., Fidanza, V., Alder, H. and Croce, C.M.  
 TITLE The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,  
 and its expression is altered in multiple human tumors  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)  
 MEDLINE 99199287  
 REFERENCE 2 (bases 1 to 9108)  
 AUTHORS Ishii, H., Baffa, R., Numata, S.I., Murakumo, Y., Rattan, S., Inoue, H.,  
 Mori, M., Fidanza, V., Alder, H. and Croce, C.M.  
 TITLE Direct Submission  
 JOURNAL Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer  
 Institute, 233S 10th street, Philadelphia, PA 19107, USA  
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GenCore version 4.5  
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(without alignments)  
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Post-processing: Minimum Match 0%  
Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
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Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
99199287
REFERENCE 2 (bases 1 to 9108)
Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
Direct Submission
Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
Institute, 233S 10th street, Philadelphia, PA 19107, USA
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Length	DB ID	Description
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25	34.6	10.0	190702 44	AC008755
26	34.4	10.0	3831 2	AF159691
27	34	9.9	4788 7	BLYSIPA
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29	34	9.9	37948 2	AF079138
30	34	9.9	43280 2	SF078289
31	34	9.9	11353 54	AC011509
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ALIGNMENTS

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RESULT 1
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LOCUS Homo sapiens FEZ1 (FEZ1) mRNA, complete cds.
DEFINITION AF123659
ACCESSION AF123659.1 GI:4572475
VERSION human.
KEYWORDS Homo sapiens
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 5492)
Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
The FEZ1 gene at chromosome 8p22 encodes a leucine-zipper protein,
and its expression is altered in multiple human tumors
Proc. Natl. Acad. Sci. U.S.A. 96 (7), 3928-3933 (1999)
99199287
2 (bases 1 to 5492)
Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
Direct Submission
Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
Institute, 2335 10th street, Philadelphia, PA 19107, USA
Location/Qualifiers
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BASE COUNT 1137 a 1704 c 1565 g 1
ORIGIN

Query Match 100.0%; Score 639; DB 40; Leu..
Best Local Similarity 100.0%; Pred. NO. 1e-79;
Matches 639; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 ggcctgagctggagggctgtgagatgagctgagcagcagcagcagcagcagcagcagcagcag 180
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QY 181 ctgcgggagaggtgagcctgctgctggagcagcagcagcagcagcagcagcagcagcagcagc 240
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QY 361 ggtctcagatgagcggcgtctgtggaagagagagagagagagagagagagagagagagag 420
DB 1681 GGCTTCAGCATGAGCGGCTCGTGTGAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1740
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QY 481 ctgcagcagctggcagctggggcagcagcggcgagcggcgagcggcgagcggcgagcggcg 540
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RESULT 2
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LOCUS Homo sapiens FEZ1 (FEZ1) gene, complete cds.
DEFINITION AF123653
ACCESSION AF123653
VERSION AF123653.1 GI:4572463
KEYWORDS human.
SOURCE Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 9108)
Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
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99199287
2 (bases 1 to 9108)
Ishii,H., Baffa,R., Numata,S.I., Murakumo,Y., Rattan,S., Inoue,H.,
Mori,M., Fidanza,V., Alder,H. and Croce,C.M.
Direct Submission
Submitted (27-JAN-1999) Immunology/Microbiology, Kimmel Cancer
Institute, 2335 10th street, Philadelphia, PA 19107, USA
Location/Qualifiers
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123659

Gencore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2000, 02:09:08 ; Search time 1236.72 Seconds  
(without alignments)  
-271.374 Million cell updates/sec

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Sequence: 1 tccgagtcacagctgcgca.....gcaggaagaagcaaatggg 345

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 882769 segs, -486395729 residues

Total number of hits satisfying chosen parameters: 1765538

Minimum DB seq length: 0  
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

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6: gb\_Ph.\*  
7: gb\_P11.\*  
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9: gb\_P13.\*  
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16: gb\_P20.\*  
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JAN 04 2001  
TECH CENTER 1600/2900

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	345	100.0	9108	40	AF123653	AF123653 Homo sapi
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3	286	82.9	1515	40	AF123655	AF123655 Homo sapi
4	286	82.9	1614	40	AF123656	AF123656 Homo sapi
5	286	82.9	1692	40	AF123657	AF123657 Homo sapi
6	286	82.9	1722	40	AF123658	AF123658 Homo sapi
7	286	82.9	1722	40	AF123659	AF123659 Homo sapi
8	106	30.7	231	40	AF123652	AF123652 Homo sapi
9	39.6	11.5	3496	1	PSEMPA	D10769 Pseudomonas
10	39.6	11.5	3496	5	E03105	E03105 DNA encodin
11	38.6	11.2	324	5	E15909	E15909 gDNA encod
12	38.6	11.2	873	1	DVUPCC3	D31702 Sulfate-red
13	36.8	10.7	25970	1	SC2H4	AL031514 Streptomy
14	36.6	10.6	1884	12	AF050418	AF050418 Mus muscu
15	36.4	10.6	4800	7	MZERAXY	M24258 Malze amylo
16	36.4	10.6	4800	7	ZMWAXY	X03935 Zea mays wa
17	35.6	10.3	151291	44	AC011772	AC011772 Homo sapi
18	35.2	10.2	2072	12	AF040746	AF040746 Mus muscu
19	35.2	10.2	4501	2	STXNLNA	M64551 Streptomyce
20	35.2	10.2	35654	1	SC7H1	AL021411 Streptomy
21	34.8	10.1	12339	8	HVU57845	U57845 Hordeum vul
22	34.8	10.1	29641	35	AC005802	AC005802 Leishman
23	34.8	10.1	186298	40	AC007860	AC007860 Homo sapi
24	34.6	10.0	5140	9	AB014541	AB014541 Homo sapi
25	34.6	10.0	190702	44	AC008755	AC008755 Homo sapi
26	34.4	10.0	3931	2	AF159691	AF159691 Myxococcu
27	34	9.9	4788	7	BLTSTPIA	M77475 Hordeum vul
28	34	9.9	9830	2	AFAGBD	L36817 Alcalaigenes
29	34	9.9	37948	2	AF079138	AF079138 Streptomy
30	34	9.9	43280	2	SFU78289	U78289 Streptomyce
31	34	9.9	113353	54	AC011509	AC011509 Homo sapi
32	33.8	9.8	674	1	DVCYTC3	X04304 Desulfovibr
33	33.8	9.8	1310	7	OSAO11078	Y0101078 Oryza sat
34	33.8	9.8	1384	7	OSAO18624	Y18624 Oryza sativ
35	33.8	9.8	1393	7	TAEI18626	Y18626 Trifolium ac
36	33.8	9.8	19830	1	SC3F9	AL023862 Streptomy
37	33.8	9.8	50394	42	AC014393	AC014393 Drosophil
38	33.6	9.7	34393	42	AC014983	AC014983 Drosophil
39	33.6	9.7	79408	45	AC021683	AC021683 Homo sapi
40	33.4	9.7	1436	8	AF033540	AF033540 Lolium pe
41	33.4	9.7	33820	2	SCCE20	AL136058 Streptomy
42	33.2	9.6	43147	1	SC4A10	AL109663 Streptomy
43	33	9.6	1240	7	DUNCBP	M23531 D. salina ma
44	33	9.6	1518	12	CPU73590	U73590 Cavia porce
45	33	9.6	2311	7	HVMAXYR	X07932 Barley mRNA

## ALIGNMENTS